Chapter 1

Introductory Chapter: Assessment and Conservation of Genetic Diversity in Plant Species

Mohamed A. El-Esawi

Additional information is available at the end of the chapter

http://dx.doi.org/10.5772/intechopen.86060

1. Genetic diversity and its assessment

Genetic diversity is the raw material that helps plant species face a wide range of daily global changes [1, 2]. It also represents the number of alternations in the genetic makeup of populations and species, which take place under various evolutionary mechanisms such as genetic drift that involves random matings of individuals within the same population, changing their allele frequencies, and founder effect that causes individuals with new genetic information leading to a new population developed from a larger one [1–3]. Genetic composition of individuals varies from one population to another due to systematic differences that emerge among individuals from different places promoting their survival and reproduction. Genetic diversity becomes more potent and quick when gene flow among populations is little such as restricted dispersal of seeds or pollens [2, 3]. Plant breeders are able to develop large amount of new productive crops that are of improved tolerance to a variety of diseases and pests as well as its enhanced ability to stand against a changing world. This depends on the volume and range of genetic variation among individuals within the same species, which allows for designing sampling programs [2, 4–6]. Accordingly, geneticists have focused on evaluating genetic differences within populations using morphological, cytological, biochemical, and molecular markers to identify the characteristics of domestication, propagation, and breeding techniques as well as conservation of plant genetic materials [2]. This work addresses various approaches related to genetic diversity in plants.

2. Biochemical markers

2.1. Storage proteins

One important output of post-transcription and translation processes is the protein, which represents the genetic DNA as well as the structural and enzymatic material of an organism's cells [2]. Genetic divergence is found to have impacts on proteins. For example, seed proteins that are of essential roles in species are tolerant to environmental occurrences. Recent approaches have employed several technologies to identify the characteristics of various plant cultivars and genotypes [2]. One quickly and precisely technology utilized for such purpose is electrophoresis. The genetic divergence was assessed within *Lathyrus sativus* through accurate electrophoretic analysis of its seed storage proteins [2, 7], suggesting its fundamental role in evaluating the relationship between taxonomy and genetics at and below the species level [2].

2.2. Isozyme markers

Isozymes, also called isoenzymes, are proteins exhibiting same catalytic and quantitative function as the enzyme but, meanwhile, they differ in their molecular forms [2]. Various alleles within a single locus are encoded by structural genes to give the allozyme, an allelic variant of the enzyme. Biological analysis of isozymes reveals significant importance, including the assessment of genetic divergence as well as phylogenetic and taxonomic relationships [2]. It also helps to investigate population genetics and developmental biology as well as to conserve the genetic resources of plants [8, 9].

3. Molecular markers

Molecular markers such as restricted fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), microsatellites (SSRs), and single-nucleotide polymorphisms (SNPs) are considered as effective and efficient tools for evaluating the genetic divergence within and among plant species [10].

3.1. Restriction fragment length polymorphism (RFLP)

RFLP is a dominant marker that involves breakages of DNA bonds at specific nucleotides by the action of enzymes called restriction endonucleases [8, 10], followed by size fractionation of digested fragments by electrophoresis technique, suggesting for these markers a key role in setting up genetic mapping as well as evaluating genetic diversity and phylogenetic relationships. RFLP markers could be a possible option to identify the characteristics of individuals, to estimate segregational analysis of progenitors as well as to evaluate genetic variation and phylogenetic relationships in the germplasms of lettuce plants, but these techniques proven to be expensive, technically complicated, and away from optimal performance [10]. Therefore, research is needed to develop low cost and more efficient molecular genetic technologies to inhibit or even limit the technical obstacles related to RFLP technique and to study the properties of genetic difference within plants [10].

3.2. Random amplified polymorphic DNA (RAPD)

RAPD, a PCR-based technique or (AP-PCR), involves the use of arbitrary short primers [8, 10] in a PCR reaction to amplify random sequences from DNA template. RAPD has proven to be a multipurpose technique utilized for constructing genetic map [11, 12], utilization in breeding approaches [13], identification of resistant genes and hybrid origin [14], and for assessing plant genetic variance by characterizing differences between populations of the similar germplasm resources [11, 12].

3.3. Amplified fragment length polymorphism (AFLP)

AFLP is a highly reproducible marker that utilizes PCR technique to amplify DNA fragments [8, 10]. It is a DNA fingerprinting-based technique that includes digestion of DNA into small fragments with the help of restriction enzymes. These fragments are ligated by adaptors complementary to their restriction sites followed by selective amplification of the newly formed subset by PCR technique [10]. Autoradiographic and fluorescence technologies are then utilized to visualize the amplified fragments on polyacrylamide gels. AFLP is proven its successful participation in identifying the characteristics of genetic diversity and relationships of plant species [8, 10, 15–20].

3.4. Microsatellites (SSRs)

Microsatellites are repetitive sequences of nitrogen bases within DNA. These repeats may be mono-, di-, tri-, tetra-, or penta-nucleotides found in eukaryotic nuclear genome [8, 10]. Microsatellites are genetically different. Therefore, they are employed in estimating genetic divergence and recognizing the relationships between plant genotypes [10, 21].

In conclusion, morphological, cytological, biochemical, and molecular markers proved useful in assessing genetic diversity levels in different plant species [22–30].

Author details

Mohamed A. El-Esawi[1,2]*

*Address all correspondence to: mohamed.elesawi@science.tanta.edu.eg

1 The Sainsbury Laboratory, University of Cambridge, Cambridge, United Kingdom

2 Botany Department, Faculty of Science, Tanta University, Tanta, Egypt

References

[1] El-Esawi MA. Assessing the genetic diversity, phylogenetic relationships, and disease resistance genes in Irish *Brassica oleracea* species [PhD thesis]. Ireland: Dublin Institute of Technology, Technological University Dublin; 2012

[2] El-Esawi MA. Taxonomic relationships and biochemical genetic characterization of *Brassica* resources: Towards a recent platform for germplasm improvement and utilization. Annual Research & Review in Biology. 2015;**8**(4):1-11

[3] Falk DA, Knapp E, Guerrant EO. Introduction to Restoration Genetics. USA: Society for Ecological Restoration; 2001

[4] El-Esawi M, Bourke P, Germaine K, Malone R. Assessment of morphological variation in Irish *Brassica oleracea* species. Journal of Agricultural Science. 2012;**4**:20-34

[5] El-Esawi MA, Sammour R. Karyological and phylogenetic studies in the genus *Lactuca* L. (Asteraceae). Cytologia. 2014;**79**:269-275

[6] Yu J, Mosjidis J, Klingler K, Woods F. Isozyme diversity in North American cultivated red clover. Crop Science. 2001;**41**:1625-1628

[7] Sammour R, Mustafa A, Badr S, Tahr W. Genetic variations in accessions of *Lathyrus sativus* L. Acta Botanica Croatica. 2007;**66**:1-13

[8] Dziechciarková M, Lebeda A, Doležalová I, Astley D. Characterization of *Lactuca* spp. germplasm by protein and molecular markers—A review. Plant, Soil and Environment. 2004;**50**:47-58

[9] Kumar P, Gupta VK, Misra AK, Modi DR, Pandey BK. Potential of molecular markers in plant biotechnology. Plant Omics Journal. 2009;**2**:141-162

[10] El-Esawi MA. Molecular genetic markers for assessing the genetic variation and relationships in *Lactuca* germplasm. Annual Research & Review in Biology. 2015;**8**(5):1-13

[11] Waycott W, Fort S. Differentiation of nearly identical germplasm accessions by a combination of molecular and morphological analyses. Genome. 1994;**85**:239-244

[12] Kesseli R, Paran I, Michelmore R. Analysis of a detailed genetic linkage map of *Lactuca sativa* (lettuce) constructed from RFLP and RAPD markers. Genetics. 1994;**136**:1435-1446

[13] Montesclaros L, Nicol N, Ubalijoro E, Leclerc-Potvin C, Ganivet L, Laliberté J. Response to potyvirus infection and genetic mapping of resistance loci to potyvirus infection in *Lactuca*. Theoretical and Applied Genetics. 1997;**94**:941-946

[14] Friesen N, Fritsch R, Bachmann K. Hybrid origin of some ornamentals of *Allium* subgenus *Melanocrommyum* verified with GISH and RAPD. Theoretical and Applied Genetics. 1997;**95**:1229-1238

[15] Koopman W, Zevenbergen M, Ronald G, van den Berg R. Species relationship in *Lactuca* S.L. (Lactuceae, *Asteraceae*) inferred from AFLP fingerprints. American Journal of Botany. 2001;**88**:1881-1887

[16] Hill M, Witsenboer H, Zabeau M, Vos P, Kesseli R, Michelmore R. PCR-based fingerprinting using AFLPs as tool for studying genetic relationship in *Lactuca* spp. Theoretical and Applied Genetics. 1996;**93**:1202-1210

[17] Johnson WC, Jackson LE, Ochoa O, van Wijk R, Peleman J, St Clair DA, et al. Lettuce, a shallow-rooted crop, and *Lactuca serriola*, its wild progenitor, differ at QTL determining

root architecture and deep soil water exploitation. Theoretical and Applied Genetics. 2000;**101**:1066-1073

[18] Jeuken M, van Wijk R, Peleman J, Lindhout P. An integrated interspecific AFLP map of lettuce (*Lactuca*) based on two *L. sativa* × *L. saligna* F2 populations. Theoretical and Applied Genetics. 2001;**103**:638-647

[19] Jeuken M, Lindhout P. *Lactuca saligna*, a non-host for lettuce downy mildew (*Bremia lactucae*), harbors a new race-specific *Dm* gene and three QTLs for resistance. Theoretical and Applied Genetics. 2002;**105**:384-391

[20] Kuang H, van Eck HJ, Sicard D, Michelmore R, Nevo E. Evolution and genetic population structure of prickly lettuce (*Lactuca serriola*) and its RGC2 resistance gene cluster. Genetics. 2008;**178**(3):1547-1558

[21] Riar D, Rustgi S, Burke I, Gill K, Yenish J. EST-SSR development from 5 *Lactuca* species and their use in studying genetic diversity among *L. serriola* biotypes. The Journal of Heredity. 2011;**102**:17-28

[22] El-Esawi MA, Germaine K, Bourke P, Malone R. Genetic diversity and population structure of *Brassica oleracea* germplasm in Ireland using SSR markers. Comptes Rendus Biologies. 2016;**339**:133-140

[23] El-Esawi MA, Germaine K, Bourke P, Malone R. AFLP analysis of genetic diversity and phylogenetic relationships of *Brassica oleracea* in Ireland. Comptes Rendus Biologies. 2016;**339**:163-170

[24] El-Esawi MA, Mustafa A, Badr S, Sammour R. Isozyme analysis of genetic variability and population structure of *Lactuca* L. germplasm. Biochemical Systematics and Ecology. 2017;**70**:73-79

[25] El-Esawi MA. Genetic diversity and evolution of *Brassica* genetic resources: From morphology to novel genomic technologies—A review. Plant Genetic Resources. 2017;**15**:388-399

[26] El-Esawi MA. SSR analysis of genetic diversity and structure of the germplasm of faba bean (*Vicia faba* L.). Comptes Rendus Biologies. 2017;**340**:474-480

[27] El-Esawi MA, Al-Ghamdi AA, Ali HM, Alayafi AA, Witczak J, Ahmad M. Analysis of genetic variation and enhancement of salt tolerance in French pea (*Pisum sativum* L.). International Journal of Molecular Sciences. 2018;**19**:2433

[28] El-Esawi MA, Alaraidh IA, Alsahli AA, Ali HM, Alayafi AA, Witczak J, et al. Genetic variation and alleviation of salinity stress in barley (*Hordeum vulgare* L.). Molecules. 2018;**23**:2488

[29] El-Esawi MA. Micropropagation technology and its applications for crop improvement. In: Anis M, Ahmad N, editors. Plant Tissue Culture: Propagation, Conservation and Crop Improvement. Singapore: Springer; 2016. pp. 523-545

[30] El-Esawi MA. Nonzygotic embryogenesis for plant development. In: Anis M, Ahmad N, editors. Plant Tissue Culture: Propagation, Conservation and Crop Improvement. Singapore: Springer; 2016. pp. 583-598

IntechOpen